Stress induced lncRNA MALAT1 in colorectal cancer health disparity

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Background: Health disparities in the lower Rio Grande Valley are well documented and can play a critical role in cancer prognosis. Chronic stress, arguably exacerbated by these disparities, can also lead to a poor outcome after diagnosis through dysregulation of molecular markers known to be involved in cancer progression, resistance, and recurrence. lncRNA have been a relatively recent point of interest in the field of cancer research and play a role in cancer initiation and progression across tissue types. We have found that lncRNA MALAT1 is stress induced through transcription factor NFATc1. Here, we propose to investigate the association of stress factors with NFATc1 and MALAT1 expression, and the role of these novel molecular drivers in CRC progression and metastasis.

Methods: CRC tissues of different ethnicities were stained using Novel Z Probe based technology (lncRNA MALAT1) and immunohistochemistry (NFATc1). Stained tissues were scanned on digital scanner and scored. CRC cell lines were profiled for MALAT1 expression using RT-PCR. Lentiviral based overexpression (SW480) and knockdown (SW620) of MALAT1 in CRC cells was performed to study proliferation, invasion, migration, and colony forming capacity

Results: MALAT1 and NFATc1 expression was scored to be high in underserved population. MALAT1 expression was lower in less aggressive SW480 cell line as compared to highly metastatic SW620 cell line. Overexpression of MALAT1 in SW480, and knockdown in SW620 resulted in changes in their oncogenic profiles.

Conclusions: Understanding the mechanistic roles molecular drivers influenced by biochemical stressors can provide pivotal information pertinent to CRC progression and metastasis.